

Genome version 5.1.3
Copyright (c) 1993 2003 Computer Ltd

OM protein - protein search, using sw model

Run on: January 16, 2003 16:40:42 : Search time 14.214 Seconds
(without alignments)
56.562 Million cell updates/sec

Title: US-09-856-070-18
Perfect score: 24
Sequence: 1 KEELM 5

Scoring table: BLQSUM62
Gapop 10 0 0 Gapext 0 5

Searched: 671580 seqs, 20604715 residues 671580
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: SP-archaea:*
- 2: SP-bacteria:*
- 3: SP-fungi:*
- 4: SP-human:*
- 5: SP-invertebrate:*
- 6: SP-mammal:*
- 7: SP-mhc:*
- 8: SP-Ornithella:*
- 9: SP-phage:*
- 10: SP-plant:*
- 11: SP-rodent:*
- 12: SP-virus:*
- 13: SP-vertebrate:*
- 14: SP-undclassified:*
- 15: SP-virus:*
- 16: SP-bacterioph:*
- 17: SP-archae:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	24	100.0	95	2	Q88671
2	24	100.0	96	17	Q8U114
3	24	100.0	97	16	Q84663
4	24	100.0	112	16	Q8XJP2
5	24	100.0	113	5	Q77163
6	24	100.0	121	16	Q8V612
7	24	100.0	124	4	Q9NTN7
8	24	100.0	135	17	Q962P1
9	24	100.0	146	4	Q9RXP7
10	24	100.0	152	4	Q9UJ22
11	24	100.0	156	4	Q9UJ28
12	24	100.0	159	4	Q9UJ27
13	24	100.0	159	4	Q9UJ26
14	24	100.0	159	16	Q8W115
15	24	100.0	161	4	Q9UK20
16	24	100.0	164	16	Q8RGP5

17	24	100.0	168	12	Q89174
18	24	100.0	168	12	Q57237
19	24	100.0	168	12	Q57237
20	24	100.0	168	12	Q89521
21	24	100.0	168	12	Q89521
22	24	100.0	174	4	Q8USN3
23	24	100.0	195	10	Q94712
24	24	100.0	196	17	Q9V307
25	24	100.0	197	17	Q59141
26	24	100.0	203	5	Q83W55
27	24	100.0	204	16	Q8K674
28	24	100.0	204	17	Q9HHA3
29	24	100.0	216	14	Q9E5F9
30	24	100.0	217	5	Q33262
31	24	100.0	226	16	Q8UKT2
32	24	100.0	273	17	Q59396
33	24	100.0	273	17	Q8U482
34	24	100.0	275	17	Q975V8
35	24	100.0	284	4	Q36MV2
36	24	100.0	300	17	Q9HKU0
37	24	100.0	305	4	Q9H278
38	24	100.0	311	4	Q9HSB6
39	24	100.0	311	14	Q9Q2P2
40	24	100.0	328	12	Q88438
41	24	100.0	329	12	Q9DKU0
42	24	100.0	338	10	Q5S261
43	24	100.0	340	10	Q82738
44	24	100.0	343	2	Q9S035
45	24	100.0	344	16	Q980C3

ALIGNMENTS

RESULT 1

068671 ID 068671 PRELIMINARY: PPT: 95 AA.
AC 068671;
DT 01-AUG-1998 (TREMblrel. 07, Created)
DI 01-AUG-1998 (TREMblrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
DE Gas vesicle protein Gvps.
GN GVPs.
OS Bacillus megaterium.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
OC Bacillaceae; Bacillus.
OX NCBI TaxID=1404;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-VT1660;
RX MEDLINE=98233742; PubMed=9573198;
RA Li N., Cannon M.C.;
RI "Gas vesicle genes identified in Bacillus megaterium and functional
RT expression in Escherichia coli.";
R1 J. Bacteriol. 180:2450-2458(1998).
DR EMBL: AF054765; AAC38410.1;
DR InterPro: IPR000638; Gas_vesicle.
DR Pfam: PF00741; Gas_vesicle; 1.
DR ProDom: PD003598; Gas_vesicle; 1.
SQ SEQUENCE 95 AA; 10422 MW; AEPALFEP927DE603B QPC64;

Query Match 100.0%; Score 24; DB 2; Length 95;

Best local similarity 100.0%; Freq. No. 1; E=0.02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Q7 1 KEELM 5
|||||
Db /5 KEELM 80

RESULT 2

Q8U114 ID Q8U114 PRELIMINARY: PPT: 96 AA.
Q8U114

```

AC 080114;
DI 01-JUN-2002 (TrEMBLrel. 21, Created)
DI 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Hypothetical protein PE1192.
GN PE1192.
OS Pyrococcus furiosus.
OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
OC Pyrococcus.
OX NCBI_TaxID=2261;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=V-1 / DSM 4648 / ATCC 4567 / DSM 8422.
RA Weiss R.B., Dunn D.M., Robb F.L., Brown J.R.
RI "The complete sequence of the Pyrococcus furiosus genome."
RL Submitted (Feb-2002) to the EMBL/GenBank/DBJ databases
DR EMBL: AF010227; AAC1316.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 96 AA: 11076 MW: 903666AERFGGQF74 CRG64;
Query Match 100.0%; Score 24; DB 17; Length 96;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
DB 17 KEELM 21

RESULT 4
084663 PRELIMINARY; PRT; 97 AA.
AC 084663;
DI 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein C1656.
GN C1656.
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=D/OW-4/EX;
RA MEDLINE=9500809; PubMed=0744136;
RA Stephens R.S., Kalman S., Lammel C., Fan J., Marathe P., Aravind L.,
RA Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
RA Davis R.W.
RI "Genome sequence of an obligate intracellular pathogen of humans:
RT Chlamydia trachomatis."
RL Science 282:754-759(1998).
DR EMBL: AF001336; AAC68251.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 97 AA: 11164 MW: 60365A5D20149F51 CRG64;
Query Match 100.0%; Score 24; DB 16; Length 97;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
DB 24 KEELM 28

RESULT 4
08XJP2 PRELIMINARY; PRT; 112 AA.
AC 08XJP2;
DI 01-MAR-2002 (TrEMBLrel. 20, Created)
DI 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DI 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Hypothetical protein GPE1714.
GN GPE1714.

```

```

OS Clostridium perfringens.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridiaceae; Clostridium.
OX NCBI_TaxID=1502;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=13 / TYPE A;
RA Shimizu T., Ohtani K., Hirakawa H., Ohshima K., Yamashita A.,
RA Shiba T., Ogasawara N., Hattori M., Kohara S., Hayashi H.
RI "Complete genome sequence of Clostridium perfringens, an anaerobic
RT flesh-eater."
FL Nucleic Acids Res. 30:1356-1365(2002).
DR EMBL: AP003191; BAB81420.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 112 AA: 12430 MW: 101094A6D81HAFFD CRG64;
Query Match 100.0%; Score 24; DB 16; Length 112;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
DB 81 KEELM 85

RESULT 5
077163 PRELIMINARY; PRT; 113 AA.
DI 077163;
AC 077163;
DI 01-NOV-1998 (TrEMBLrel. 08, Created)
DI 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DI 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE App-ribosylation factor (Fragment).
GN App.
OS Entamoeba invadens.
OC Eukaryota; Entamoebidae; Entamoeba.
OX NCBI_TaxID=33085;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=IP-1;
RA MEDLINE=99270976; PubMed=10338523;
RA Ghosh S.K., Field J., Frisardi M., Rosenthal B., Mai Z., Rogers R.,
RA Samuelson J.
RI "Chitinase secretion by encysting Entamoeba invadens and transfected
RT Entamoeba histolytica trophozoites: localization of secretory
RT vesicles, endoplasmic reticulum, and Golgi apparatus."
RL Infect. Immun. 67:3073-3081(1999).
DR EMBL: AF082518; AAC64064.1; -.
DR HSSP; P32889; IRRF.
DR InterPro; IPR000251; ARF_family.
DR InterPro; IPR002046; Sar1_GTPBP.
DR Pfam; PF00025; arf; 1.
DR PRINTS; PP00328; SAR1GTPBP.
DR SMART; SM00177; ARF; 1.
FT NON_TER 1
FT NON_TER 113
SQ SEQUENCE 113 AA: 12991 MW: 64A1CF5451D1M46 CRG64;
Query Match 100.0%; Score 24; DB 5; Length 113;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
DB 86 KEELM 90

RESULT 6
08Y612 PRELIMINARY; PRT; 121 AA.
DI 08Y612;
AC 08Y612;
DI 01-MAR-2002 (TrEMBLrel. 20, Created)

```

DI 01-MAR-2002 (TREMBlrel. 20, last sequence update)
 DI 01-MAR-2002 (TREMBlrel. 20, last annotation update)
 GN LMO1890.
 OS Listeria monocytogenes.
 OC Bacteria: Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Listeriaceae; Listeria.
 OX NCHI_TaxID=1639;
 RN [1]
 PP SEQUENCE FROM N.A.
 PC STRAIN-EGD-E / SEPOVAP 1/2A;
 RX MEDLINE=21537279; PubMed=11679669;
 RA Glaser P., Frangeul L., Buchrieser C., Rusniok C., Amend A.,
 RA Baquero F., Berche P., Blocker H., Brandt P., Chakraborty T.,
 RA Charif A., Chetoui F., Couve E., de Lencastre A., Dehoux P.,
 RA Domann E., Dominguez-Bernal G., Duchaud F., Duran L., Dussartel O.,
 PA Entian K.-D., Fshih H., Garcia-del Portillo F., Garido P.,
 RA Gautier L., Geisel W., Gomez Lopez N., Hain T., Hauf J., Jackson P.,
 RA Jones L.-M., Kastrup U., Kretz J., Kuhn M., Kuntz P., Kurapkar G.,
 RA Madico E., Maitournam A., Mata Vicente J., Ng E., Nedjari H.,
 RA Nordstiek G., Novella S., de Pablo B., Perez-Diaz J.-C., Purcell R.,
 RA Remmel B., Rose M., Schlutner T., Simoes N., Tierrez A.,
 RA Vazquez-Boland J. A., Voss H., Wehland J., Gessart F.,
 RT "Comparative genomics of *Listeria* species";
 RL Science 294:849-852(2001)
 DR EMBL: AL591981; CAC95968.1; -;
 DR LocusList: LMO01890; -;
 KW Hypothetical protein. Complete proteome.
 SQ SEQUENCE 121 AA; 14517 MW; 5EE201A36C170248 CRC64;

Query Match 100.0%; Score 24; DB 16; Length 121;
 Best Local Similarity 100.0%; Pred. No. 1 8e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 DB 117 KEELM 121
 |||||

RESULT 7
 Q9NTN7
 ID Q9NTN7 PRELIMINARY: PPT; 124 AA.
 AC Q9NTN7;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
 DI 01-SEP-2001 (TREMBlrel. 19, last annotation update)
 DE DJ207F6.1 (Novel nucleolar protein NOP56 like protein)
 DF (Fragment)
 GN DJ207F6.1.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCHI_TaxID=9606;
 RN [1]
 PP SEQUENCE FROM N.A.
 RA Griffiths G.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL13258; CAB92070.1; -;
 DR InterPro: IPR000873; AMP-Bind.
 DR PROSITE: PS00455; AMP_HINGING; UNKNOWN_1.
 FT NON_TER 1
 SQ SEQUENCE 124 AA; 13898 MW; 263A046C3560622C CRC64;

Query Match 100.0%; Score 24; DB 4; Length 124;
 Best Local Similarity 100.0%; Pred. No. 1 4e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 DB 44 KEELM 48
 |||||

RESULT 8

C96ZEL
 ID Q96ZEL PRELIMINARY: PPT; 135 AA.
 AC Q96ZEL;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
 DI 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Putative transcriptional regulator.
 GN S01890.
 OS Sulfolobus tokodaii.
 OC Archaea; Crenarchaeota; Thermoprotei; Sulfolobales; Sulfolobaceae;
 OX NCHI_TaxID=111955;
 RN [1]
 PP SEQUENCE FROM N.A.
 PC STRAIN-JCM 10545 / 7;
 RX PubMed=11572479;
 RA Kawarabayashi Y., Hino Y., Horikawa H., Jinno K., Takahashi M.,
 RA Sakino M., Baba S.-I., Anai A., Koshiji H., Haseyama A., Fukui S.,
 RA Nagai Y., Nishijima K., Otsuka P., Nakazawa H., Takamiya M., Kato Y.,
 RA Yoshizawa T., Tanaka T., Kudo Y., Yamazaki I., Koshida N., Oguchi A.,
 RA Aoki K. I., Masuda S., Yanaqili M., Nishimura M., Yamagishi A.,
 RA Oshima T., Kikuchi H.;
 RT "Complete genome sequence of an aerobic thermophilic
 KT Crenarchaeon, *Sulfolobus tokodaii* strain 7";
 RL DNA Res. 8:123-140(2001).
 DR EMBL: AP000044; HAR66984.1; -;
 KW Hypothetical protein. Complete proteome.
 SQ SEQUENCE 135 AA; 15654 MW; 9d18AA9B4502FAC2 CRC64;

Query Match 100.0%; Score 24; DB 17; Length 135;
 Best Local Similarity 100.0%; Pred. No. 2e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 DB 103 KEELM 107
 |||||

RESULT 9
 Q9BRX7
 ID Q9BRX7 PRELIMINARY: PPT; 146 AA.
 AC Q9BRX7;
 DT 01-JUN-2001 (TREMBlrel. 17, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, last sequence update)
 DI 01-JUN-2002 (TREMBlrel. 21, last annotation update)
 DE Hypothetical 14 kDa protein (uncloned) (Fract. 102 W0117517).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCHI_TaxID=9606;
 RN [1]
 PP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 RN [2]
 PP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RA Strausberg R.;
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 RA Strausberg R.;
 DR EMBL: BC005872; AAH05872.1; -;
 DR EMBL: BC011498; AAH11498.1; -;
 DP InterPro: IPR000286; His_deacetylase.
 DR Pfam: PF00850; Hist_deacetyl_1;
 KW Hypothetical protein.
 SQ SEQUENCE 146 AA; 16439 MW; 6A2C126D1F836B CRC64;

Query Match 100.0%; Score 24; DB 4; Length 146;
 Best Local Similarity 100.0%; Pred. No. 2.2e-02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KEELM 5
 DB 1111

```

Db      148 KEELM 142

RESULT 10
Q9UJZ4
ID      Q9UJZ4      PRELIMINARY:      PRT:      152 AA.
AC      Q9UJZ4
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DI      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE      01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE      Cytoovillin 2 (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-BRAIN;
RA      Chen Z.C., Fadiel A., Nattoli F.;
RL      "Mutation of cytoovillin gene in glioblastoma.";
RL      Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF190059; AA03158.1; -.
DR      InterPro; IPR000299; Band_4.1.
DR      InterPro; IPR000798; Ez/rad/moesin.
DR      Pfam; PF00769; ERM; 1.
DR      PROSITE; PS50057; BAND_41_3; 1.
FT      NON_TER 1
FT      NON_TER 152
SQ      SEQUENCE 152 AA: 19416 MW: 8709817DDJB9291 CRC64;

Query Match      100.0%; Score 24; DB 4; Length 152;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KEELM 5
      [1111]

Db      144 KEELM 148

RESULT 11
Q9UJZ8
ID      Q9UJZ8      PRELIMINARY:      PRT:      156 AA.
AC      Q9UJZ8
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DI      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE      01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE      Ezrin (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-BRAIN;
RA      Chen Z.C., Fadiel A., Nattoli F.;
RL      "Mutation of ezrin gene in cancer.";
RL      Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF188896; AA03154.1; -.
DR      InterPro; IPR000299; Band_4.1.
DR      InterPro; IPR000798; Ez/rad/moesin.
DR      Pfam; PF00769; ERM; 1.
DR      PROSITE; PS50057; BAND_41_3; 1.
FT      NON_TER 1
FT      NON_TER 156
SQ      SEQUENCE 156 AA: 19642 MW: 15055AA684A293A6 CRC64;

Query Match      100.0%; Score 24; DB 4; Length 156;
Best Local Similarity 100.0%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KEELM 5
      [1111]

```

```

Db      148 KEELM 152

RESULT 12
Q9UJZ7
ID      Q9UJZ7      PRELIMINARY:      PRT:      158 AA.
AC      Q9UJZ7
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DI      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE      01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE      Ezrin (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Ovary;
RA      Chen Z.C., Fadiel A., Nattoli F.;
RL      "Ezrin gene mutation in ovarian cancer.";
RL      Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF188897; AA03155.1; -.
DR      InterPro; IPR000299; Band_4.1.
DR      InterPro; IPR000798; Ez/rad/moesin.
DR      Pfam; PF00769; ERM; 1.
DR      PROSITE; PS50057; BAND_41_3; 1.
FT      NON_TER 1
FT      NON_TER 158
SQ      SEQUENCE 158 AA: 19086 MW: 86592F1HC6F2957E CRC64;

Query Match      100.0%; Score 24; DB 4; Length 158;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KEELM 5
      [1111]

Db      147 KEELM 151

RESULT 13
Q9UJZ6
ID      Q9UJZ6      PRELIMINARY:      PRT:      159 AA.
AC      Q9UJZ6
DT      01-MAY-2000 (TrEMBLrel. 13, Created)
DI      01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE      01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE      Ezrin (Fragment).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-BRAIN;
RA      Fadiel A., Chen Z.C., Nattoli F.;
RL      "Mutation of ezrin gene in cancer.";
RL      Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AF189213; AA03156.1; -.
DR      InterPro; IPR000299; Band_4.1.
DR      InterPro; IPR000798; Ez/rad/moesin.
DR      Pfam; PF00769; ERM; 1.
DR      PROSITE; PS50057; BAND_41_3; 1.
FT      NON_TER 1
FT      NON_TER 159
SQ      SEQUENCE 159 AA: 19234 MW: 70398488B7BA70FA CRC64;

Query Match      100.0%; Score 24; DB 4; Length 159;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 KEELM 5
      [1111]

Db      147 KEELM 151

```

Search completed: January 16, 2003, 16:55:41
Job Time : 20.2143 secs

RESULT 14

Q8RII5 Q8RII5 PRELIMINARY: PRT: 159 AA.
AC Q8RII5
DI 01-JUN-2002 (FEMBLrel_21, Created)
DI 01-JUN-2002 (FEMBLrel_21, last sequence update)
DE Competence protein.
GN FN1611.
OS Fusobacterium nucleatum (subsp. nucleatum).
OC Bacteria; Fusobacteria; Fusobacterium.
OX NCBI_TaxID=76856;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 25586;
RX MEDLINE-21886394; PubMed-11889109;
RA Kapral V., Anderson J., Ivancova N., Reznik G., Los T., Lykidis A.,
RA Bhattacharya A., Hartman A., Gardner W., Grechkin G., Zhu L.,
RA Vasileva O., Chu L., Kogan Y., Chaga O., Goltsman E., Hernal A.,
RA Larsen N., D'Souza M., Walunas T., Pusch G., Haselkorn R.,
RA Fonstein M., Kyripides N., Overbeek R.;
RT "Genome sequence and analysis of the oral bacterium Fusobacterium
nucleatum strain ATCC 25586.";
PI J. Bacteriol. 184:2005-2018(2002).
PK EMBL: AF010469; AAL93726.1; -.
KW Complete proteome.
SQ SEQUENCE 159 AA: 18634 MW: 18159460363DB6 CRC64;

Query Match 100.0%; Score 24; DH 16; Length 159;
Host local Similarity 100.0%; Pred.No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
|
|
|
|
DB 25 KEELM 29

RESULT 15

Q90K20 Q90K20 PRELIMINARY: PRT: 161 AA.
AC Q90K20;
DI 01-MAY-2000 (FEMBLrel_13, Created)
DI 01-MAY-2000 (FEMBLrel_13, last sequence update)
DI 01-MAR-2002 (FEMBLrel_20, last annotation update)
DE Ezrin (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-PLACENTA;
RA Chen Z.C., Fadiel A., Naftolin F.;
RT "Mutation analysis of ezrin gene in cancer cells.";
RI Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF187552; AAD56713.1; -.
DR InterPro: IPR000294; Band_4 1.
DR Pfam: PF00373; Band_41; 1.
DR Pfam: PF00769; ERW; 1.
DR PROSITE: PS50057; BAND_41_3; 1.
FT NON_TER 1 161
FT NON_TER 161 161
SQ SEQUENCE 161 AA: 19436 MW: 510648910E017099 CRC64;

Query Match 100.0%; Score 24; DB 4; Length 161;
Host local Similarity 100.0%; Pred.No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KEELM 5
|
|
|
|
DB 153 KEELM 157

